

(e) a fifth program code for linking the information for display to the related peak in the molecular topography.

Please cancel Claims 1 and 22 without prejudice towards prosecution in a continuation or divisional application.

REMARKS

Reconsideration of this application is requested in view of the foregoing amendment and the following remarks.

Claims 1 to 3 and 5 to 24 have been pending in the instant application. By the foregoing amendment, Claims 2, 3, 5, 6, 11, 12, 23, and 24 have been amended and Claims 1 and 22 have been cancelled without prejudice towards further prosecution in a continuation or divisional application. Accordingly, upon entry of this amendment, Claims 2 to 3 and 5 to 21, 23, and 24 will remain pending in this application.

The Applicants' representative kindly thank Examiner Marschel for indicating that Claims 8 to 10 and 13 to 21 are allowed and that Claims 3, 6, 12, and 23 would be allowable if rewritten in independent form including all the limitations of the base claim and any intervening claims. Claims 3, 6, 12, and 23 have been so amended. The Applicants' representative notes that Claim 7 as depending from Claim 6 would now be allowed, as well. The Applicants' representative kindly thank Examiner Marschel for withdrawing then rejections and objections from the previous Office Actions and for withdrawing the finality of the Office Action.

The above amendments to the claims have been made for purposes of more clearly depicting the present invention.

The Rejection of Claims 1, 2, 5, 11, 22, and 24 Under 35 U.S.C. § 103(a):

The Examiner has rejected Claims 1, 2, 5, 11, 22, and 24 under 35 U.S.C. § 103(a) as being unpatentable over U.S. Patent No. 5,811,231, issued to Farr et al.(hereinafter Farr). This rejection has been obviated by appropriate amendment and, where not obviated, is respectfully traversed.

Farr discloses the "measure[ment of] transcription or translation levels from genes linked to native eukaryotic stress promoters." (Abstract.) The Examiner asserts that Figures 1 to 11 of Farr display said gene expression in a perspective 3-dimensional manner with parameters for each expression level in the third dimension. One characteristic parameter is concentration of a compound which may alter gene expression and another is the stress promoter being evaluated regarding the gene expression.

However, Claims 2 and 24, as now presented, (and Claim 5, which now depends from Claim 2) further requires generating a file containing information for display relating to a peak in the molecular topology, and linking the information for display to the related peak in the molecular topography. Such features are neither disclosed nor suggested in Farr.

Further, Claim 11 is directed to a method in a computer system for displaying differences in gene expression, comprising: (1) for each of two gene expression profiles to be compared generating a molecular topography according to claim 1, (2) for each position in the two co-ordinate space subtracting the measure of quantity in the first profile from the measure of quantity in the second profile; (3) for each position, generating a peak for display from the difference; and (4) displaying the respective difference peak at each of the positions in the two co-ordinate space. Such features are neither disclosed nor suggested in Farr.

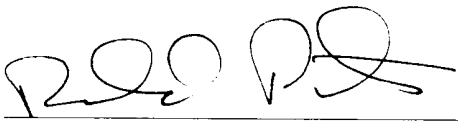
Accordingly, it is respectfully submitted that the cited reference of Farr would not suggest the present invention when applied as a reference against the invention of the present claims.

For all of the above reasons, Applicants submit that this application is now in condition for allowance. Prompt issuance of a Notice of Allowance is earnestly solicited.

Should the Examiner determine that any further action is necessary to place this application into better form, the Examiner is encouraged to telephone Applicants' undersigned representative at the number listed below. In addition, if any additional fees are required in connection with the filing of this response, the Commissioner is hereby authorized to charge the same to Deposit Account No. 501458.

Respectfully submitted,

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Version With Markings To Show Changes Made

2 A method in a computer system for analyzing and displaying data on gene expression in a molecular topography, comprising:

(a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i) a first value for a first polynucleotide characteristic,

(ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii) a third value that is a measure of the quantity of the polynucleotide;

(b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression [. A method in a computer system for analyzing and displaying data on gene expression in a molecular topography according to claim 1, and] further comprising:

(d) generating a file containing information for display relating to a peak in the molecular topology, and

(e) linking the information for display to the related peak in the molecular topography.

3. [The] A method [according to claim 1.] in a computer system for analyzing an displaying data on gene expression in a molecular topography, comprising:

(a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i) a first value for a first polynucleotide characteristic,

(ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii) a third value that is a measure of the quantity of the polynucleotide;

(b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

wherein: (i) the first characteristic is a sequence identifier, and (ii) the second characteristic is a measure of size.

5. The method of [claim] Claim [1] 2, wherein the polynucleotides are cDNAs or fragments thereof.

6. [The] A method [according to claim 5] in a computer system for analyzing an displaying data on gene expression in a molecular topography, comprising:

(a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

- (i) a first value for a first polynucleotide characteristic,
 - (ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and
 - (iii) a third value that is a measure of the quantity of the polynucleotide;
 - (b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and
 - (c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,
- wherein the polynucleotides are cDNAs or fragments thereof, and
- wherein the polynucleotides are 3'-end fragments of restriction enzyme cleaved cDNAs.

11. A method in a computer system for displaying differences in gene expression, comprising:

- (1) for each of two gene expression profiles to be compared generating a molecular topography according to a method in a computer system for analyzing and displaying data on gene expression in a molecular topography, comprising:
 - (a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:
 - (i) a first value for a first polynucleotide characteristic,
 - (ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and
 - (iii) a third value that is a measure of the quantity of the polynucleotide;

(b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

(2) for each position in the two co-ordinate space subtracting the measure of quantity in the first profile from the measure of quantity in the second profile;

(3) for each position, generating a peak for display from the difference; and

(4) displaying the respective difference peak at each of the positions in the two co-ordinate space.

12. [The] A method [according to claim 11] in a computer system for displaying differences in gene expression, comprising:

(1) for each of two gene expression profiles to be compared generating a molecular topography according to a method, comprising:

(a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i) a first value for a first polynucleotide characteristic,

(ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii) a third value that is a measure of the quantity of the polynucleotide;

(b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression,

(2) for each position in the two co-ordinate space subtracting the measure of quantity in the first profile from the measure of quantity in the second profile;

(3) for each position, generating a peak for display from the difference; and

(4) displaying the respective difference peak at each of the positions in the two co-ordinate space,

wherein differences are displayed only if they meet or exceed a threshold value.

23. [The] A method [according to claim 22] in a computer system for displaying a series of in gene expression profiles in a molecular movie, comprising:

(1) generating a plurality of molecular topographies according to a method, comprising:

(a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i) a first value for a first polynucleotide characteristic,

(ii) a second value for a second polynucleotide-characteristic different from said first characteristic, and

(iii) a third value that is a measure of the quantity of the polynucleotide;

(b) calculating for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

(c) displaying the peak for each polynucleotide at the calculated position for the polynucleotide in the display, the resulting display representing thereby a molecular topography of gene expression, and

(2) displaying the molecular topographies in succession,

wherein the molecular topographies are delta plots.

24. A computer program product, usable in a computer system, for analyzing and displaying gene expression in a molecular topography, the computer program product comprising:

a first program code that generates a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i) a first value for a first polynucleotide characteristic,

(ii) a second value for a second polynucleotide- characteristic different from said first characteristic, and

(iii) a third value that is a measure of the quantity of the polynucleotide; a second program code that calculates for each polynucleotide from the first and second values a position, and from the third value a peak at that position in a multi-dimensional display space; and

a third program code that displays the peak for each polynucleotide at the calculated position for the polynucleotide in a display, the resulting display resulting thereby a molecular topography of gene expression, and further comprising

(d) a fourth program code for generating a file containing information for display relating to a peak in the molecular topology, and

(e) a fifth program code for linking the information for display to the related peak in the molecular topography.